

RAW SEQUENCE LISTING

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Application Serial Number: 10/501,756
Source: PCT
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PATENT APPLICATION: US/10/501,756

DATE: 01/04/2005
TIME: 14:46:48

PCT

Input Set : D:\180-137 PCT.ST25.txt
Output Set: N:\CRF4\01042005\J501756.raw

3 <110> APPLICANT: Duke University
 4 Chuan-Yuan, Li
 5 Xiuwu, Zhang
 7 <120> TITLE OF INVENTION: GENERATION OF RECOMBINANT ADENO-ASSOCIATED VIRAL VECTORS BY
 A
 8 COMPLETE ADENOVIRUS-MEDIATED APPROACH
 10 <130> FILE REFERENCE: 180/137
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/501,756
 C--> 12 <141> CURRENT FILING DATE: 2004-07-16
 12 <150> PRIOR APPLICATION NUMBER: US 60/349,532
 13 <151> PRIOR FILING DATE: 2002-01-18
 15 <160> NUMBER OF SEQ ID NOS: 22
 17 <170> SOFTWARE: PatentIn version 3.2
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1611
 21 <212> TYPE: DNA
 22 <213> ORGANISM: adeno-associated virus 2
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (1)..(1611)
 29 <400> SEQUENCE: 1
 30 atg ccg ggg ttt tac gag att gtg att aag gtc ccc agc gac ctt gac 48
 31 Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 32 1 5 10 15
 34 gag cat ctg ccc ggc att tct gac agc ttt gtg aac tgg gtg gcc gag 96
 35 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 36 20 25 30
 38 aag gaa tgg gag ttg ccg cca gat tct gac atg gat ctg aat ctg att 144
 39 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
 40 35 40 45
 42 gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttt ctg 192
 43 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
 44 50 55 60
 46 acg gaa tgg cgc cgt gtg agt aag gcc ccg gag gcc ctt ttc ttt gtg 240
 47 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
 48 65 70 75 80
 50 caa ttt gag aag gga gag agc tac ttc cac atg cac gtg ctc gtg gaa 288
 51 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
 52 85 90 95
 54 acc acc ggg gtg aaa tcc atg gtt ttg gga cgt ttc ctg agt cag att 336
 55 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
 56 100 105 110
 58 cgc gaa aaa ctg att cag aga att tac cgc ggg atc gag ccg act ttg 384
 59 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu

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60	115	120	125	
62	cca aac tgg ttc gcg gtc aca aag acc aga aat ggc gcc gga ggc ggg			432
63	Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly			
64	130	135	140	
66	aac aag gtg gtg gat gag tgc tac atc ccc aat tac ttg ctc ccc aaa			480
67	Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys			
68	145	150	155	160
70	acc cag cct gag ctc cag tgg gcg tgg act aat atg gaa cag tat tta			528
71	Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu			
72	165	170	175	
74	agc gcc tgt ttg aat ctc acg gag cgt aaa cgg ttg gtg gcg cag cat			576
75	Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His			
76	180	185	190	
78	ctg acg cac gtg tcg cag acg cag gag cag aac aaa gag aat cag aat			624
79	Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn			
80	195	200	205	
82	ccc aat tct gat gcg ccg gtg atc aga tca aaa act tca gcc agg tac			672
83	Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr			
84	210	215	220	
86	atg gag ctg gtc ggg tgg ctc gtg gac aag ggg att acc tcg gag aag			720
87	Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys			
88	225	230	235	240
90	cag tgg atc cag gag gac cag gcc tca tac atc tcc ttc aat gcg gcc			768
91	Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala			
92	245	250	255	
94	tcc aac tcg cgg tcc caa atc aag gct gcc ttg gac aat gcg gga aag			816
95	Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys			
96	260	265	270	
98	att atg agc ctg act aaa acc gcc ccc gac tac ctg gtg ggc cag cag			864
99	Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln			
100	275	280	285	
102	ccc gtg gag gac att tcc agc aat cgg att tat aaa att ttg gaa cta			912
103	Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu			
104	290	295	300	
106	aac ggg tac gat ccc caa tat gcg gct tcc gtc ttt ctg gga tgg gcc			960
107	Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala			
108	305	310	315	320
110	acg aaa aag ttc ggc aag agg aac acc atc tgg ctg ttt ggg cct gca			1008
111	Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala			
112	325	330	335	
114	act acc ggg aag acc aac atc gcg gag gcc ata gcc cac act gtg ccc			1056
115	Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro			
116	340	345	350	
118	ttc tac ggg tgc gta aac tgg acc aat gag aac ttt ccc ttc aac gac			1104
119	Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp			
120	355	360	365	
122	tgt gtc gac aag atg gtg atc tgg tgg gag gag ggg aag atg acc gcc			1152
123	Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala			
124	370	375	380	

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126 aag gtc gtg gag tcg gcc aaa gcc att ctc gga gga agc aag gtg cgc	1200
127 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg	
128 385 390 395 400	
130 gtg gac cag aaa tgc aag tcc tcg gcc cag ata gac ccg act ccc gtg	1248
131 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val	
132 405 410 415	
134 atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac tca	1296
135 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser	
136 420 425 430	
138 acg acc ttc gaa cac cag cag ccg ttg caa gac ccg atg ttc aaa ttt	1344
139 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe	
140 435 440 445	
142 gaa ctc acc cgc cgt ctg gat cat gac ttt ggg aag gtc acc aag cag	1392
143 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln	
144 450 455 460	
146 gaa gtc aaa gac ttt ttc cgg tgg gca aag gat cac gtg gtt gag gtg	1440
147 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val	
148 465 470 475 480	
150 gag cat gaa ttc tac gtc aaa aag ggt gga gcc aag aaa aga ccc gcc	1488
151 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala	
152 485 490 495	
154 ccc agt gac gca gat ata agt gag ccc aaa ccg gtg cgc gag tca gtt	1536
155 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val	
156 500 505 510	
158 gcg cag cca tcg acg tca gac gcg gaa gct tcg atc aac tac gca gac	1584
159 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp	
160 515 520 525	
162 aga ttg gct cga gga cac tct ctc tga	1611
163 Arg Leu Ala Arg Gly His Ser Leu	
164 530 535	
167 <210> SEQ ID NO: 2	
168 <211> LENGTH: 536	
169 <212> TYPE: PRT	
170 <213> ORGANISM: adeno-associated virus 2	
172 <400> SEQUENCE: 2	
174 Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp	
175 1 5 10 15	
178 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu	
179 20 25 30	
182 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile	
183 35 40 45	
186 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu	
187 50 55 60	
190 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val	
191 65 70 75 80	
194 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu	
195 85 90 95	
198 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile	
199 100 105 110	

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202 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
203 115 120 125
206 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
207 130 135 140
210 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
211 145 150 155 160
214 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
215 165 170 175
218 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
219 180 185 190
222 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
223 195 200 205
226 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
227 210 215 220
230 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
231 225 230 235 240
234 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
235 245 250 255
238 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
239 260 265 270
242 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
243 275 280 285
246 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
247 290 295 300
250 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
251 305 310 315 320
254 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
255 325 330 335
258 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
259 340 345 350
262 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
263 355 360 365
266 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
267 370 375 380
270 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
271 385 390 395 400
274 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
275 405 410 415
278 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
279 420 425 430
282 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
283 435 440 445
286 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
287 450 455 460
290 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
291 465 470 475 480
294 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
295 485 490 495
298 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

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299	500	505	510	
302	Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp			
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307	530	535		
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311	<211> LENGTH: 1866			
312	<212> TYPE: DNA			
313	<213> ORGANISM: adeno-associated virus 2			
316	<220> FEATURE:			
317	<221> NAME/KEY: CDS			
318	<222> LOCATION: (1)..(1866)			
320	<400> SEQUENCE: 3			
321	atg ccg ggg ttt tac gag att gtg att aag gtc ccc agc gac ctt gac			48
322	Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp			
323	1 5 10 15			
325	ggg cat ctg ccc ggc att tct gac agc ttt gtg aac tgg gtg gcc gag			96
326	Gly His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu			
327	20 25 30			
329	aag gaa tgg gag ttg ccg cca gat tct gac atg gat ctg aat ctg att			144
330	Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile			
331	35 40 45			
333	gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttt ctg			192
334	Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu			
335	50 55 60			
337	acg gaa tgg cgc cgt gtg agt aag gcc ccg gag gcc ctt ttc ttt gtg			240
338	Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val			
339	65 70 75 80			
341	caa ttt gag aag gga gag agc tac ttc cac atg cac gtg ctc gtg gaa			288
342	Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu			
343	85 90 95			
345	acc acc ggg gtg aaa tcc atg gtt ttg gga cgt ttc ctg agt cag att			336
346	Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile			
347	100 105 110			
349	cgc gaa aaa ctg att cag aga att tac cgc ggg atc gag ccg act ttg			384
350	Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu			
351	115 120 125			
353	cca aac tgg ttc gcg gtc aca aag acc aga aat ggc gcc gga ggc ggg			432
354	Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly			
355	130 135 140			
357	aac aag gtg gtg gat gag tgc tac atc ccc aat tac ttg ctc ccc aag			480
358	Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys			
359	145 150 155 160			
361	acc cag cct gaa ctg cag tgg gcg tgg act aat atg gaa cag tat tta			528
362	Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu			
363	165 170 175			
365	agc gcc tgt ttg aat ctc acg gag cgt aaa cggtt gtc gcg cag cat			576
366	Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His			
367	180 185 190			

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date